



PCT

RAW SEQUENCE LISTING

DATE: 10/27/2004

PATENT APPLICATION: US/10/511,657

TIME: 15:26:56

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\10272004\J511657.raw

3 <110> APPLICANT: Lynkeus Biotech GmbH
 5 <120> TITLE OF INVENTION: Means and Methods for the Specific Modulation of Target
 Genes in the CNS
 6 and the Eye and Methods for Their Identification
 W--> 7 <130> FILE REFERENCE: LY01A04/P-WO
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/511,657
 C--> 9 <141> CURRENT FILING DATE: 2004-10-18
 9 <150> PRIOR APPLICATION NUMBER: EP02008761.5
 10 <151> PRIOR FILING DATE: 2002-04-18
 12 <150> PRIOR APPLICATION NUMBER: US 60/431,173
 13 <151> PRIOR FILING DATE: 2002-12-05
 15 <160> NUMBER OF SEQ ID NOS: 10
 17 <170> SOFTWARE: PatentIn version 3.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 2500
 21 <212> TYPE: DNA
 22 <213> ORGANISM: homo sapiens
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (25)..(2097)
 27 <223> OTHER INFORMATION: Homo sapiens cyclic nucleotide gated channel alpha 1
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 32 Met Lys Leu Ser Met Lys Asn Asn Ile
 33 1 5
 35 atc aat aca cag cag tct ttt gta acc atg ccc aat gtg att gta cca 99
 36 Ile Asn Thr Gln Gln Ser Phe Val Thr Met Pro Asn Val Ile Val Pro
 37 10 15 20 25
 39 gat att gaa aag gaa ata cga agg atg gaa aat gga gca tgc agc tcc 147
 40 Asp Ile Glu Lys Glu Ile Arg Arg Met Glu Asn Gly Ala Cys Ser Ser
 41 30 35 40
 43 ttt tct gag gat gat gac agt gcc tat aca tct gaa gaa tca gag aat 195
 44 Phe Ser Glu Asp Asp Asp Ser Ala Tyr Thr Ser Glu Glu Ser Glu Asn
 45 45 50 55
 47 gaa aac cct cat gca agg ggt tcc ttt agt tat aag tca ctc aga aag 243
 48 Glu Asn Pro His Ala Arg Gly Ser Phe Ser Tyr Lys Ser Leu Arg Lys
 49 60 65 70
 51 gga gga cca tca cag agg gag cag tac ctg cct ggt gcc att gcc att 291
 52 Gly Gly Pro Ser Gln Arg Glu Gln Tyr Leu Pro Gly Ala Ile Ala Ile
 53 75 80 85
 55 ttt aat gtg aac aac agc agc aat aag gac cag gaa cca gag gaa aaa 339
 56 Phe Asn Val Asn Asn Ser Ser Asn Lys Asp Gln Glu Pro Glu Glu Lys
 57 90 95 100 105
 59 aag aaa aag aaa aaa gaa aag aag agc aag tca gat gat aaa aac gaa 387

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60 Lys Lys Lys Lys Lys Glu Lys Lys Ser Lys Ser Asp Asp Lys Asn Glu
61          110          115          120
63 aat aaa aac gac cca gag aag aaa aag aag aaa aag gac aaa gag aag      435
64 Asn Lys Asn Asp Pro Glu Lys Lys Lys Lys Lys Lys Asp Lys Glu Lys
65          125          130          135
67 aaa aag aaa gag gag aaa agc aaa gat aag aaa gaa cac cac aag aaa      483
68 Lys Lys Lys Glu Glu Lys Ser Lys Asp Lys Lys Glu His His Lys Lys
69          140          145          150
71 gaa gtt gtg gtt att gat ccc tcg gga aac aca tat tac aac tgg ctg      531
72 Glu Val Val Val Ile Asp Pro Ser Gly Asn Thr Tyr Tyr Asn Trp Leu
73          155          160          165
75 ttt tgc atc aca tta cct gtt atg tac aac tgg aca atg gtt att gcc      579
76 Phe Cys Ile Thr Leu Pro Val Met Tyr Asn Trp Thr Met Val Ile Ala
77 170          175          180          185
79 aga gca tgt ttt gat gaa ctt caa tct gat tac cta gaa tat tgg ctc      627
80 Arg Ala Cys Phe Asp Glu Leu Gln Ser Asp Tyr Leu Glu Tyr Trp Leu
81          190          195          200
83 att ttg gat tac gta tca gac ata gtc tat tta atc gat atg ttt gta      675
84 Ile Leu Asp Tyr Val Ser Asp Ile Val Tyr Leu Ile Asp Met Phe Val
85          205          210          215
87 cga aca agg aca ggt tac cta gaa caa gga ctg ctg gta aag gaa gaa      723
88 Arg Thr Arg Thr Gly Tyr Leu Glu Gln Gly Leu Leu Val Lys Glu Glu
89          220          225          230
91 ctt aaa ctc ata aat aaa tat aaa tcc aac ttg caa ttt aaa ctt gat      771
92 Leu Lys Leu Ile Asn Lys Tyr Lys Ser Asn Leu Gln Phe Lys Leu Asp
93          235          240          245
95 gtt ctg tca ctg ata cca act gat ttg ctg tat ttt aag tta ggg tgg      819
96 Val Leu Ser Leu Ile Pro Thr Asp Leu Leu Tyr Phe Lys Leu Gly Trp
97 250          255          260          265
99 aac tat cca gaa att aga tta aac agg ttg tta cgg ttc tct cgt atg      867
100 Asn Tyr Pro Glu Ile Arg Leu Asn Arg Leu Leu Arg Phe Ser Arg Met
101          270          275          280
103 ttt gag ttc ttc cag aga aca gaa aca agg aca aac tat cca aac atc      915
104 Phe Glu Phe Phe Gln Arg Thr Glu Thr Arg Thr Asn Tyr Pro Asn Ile
105          285          290          295
107 ttc agg att tcc aac ctt gtt atg tat atc gtc atc att atc cac tgg      963
108 Phe Arg Ile Ser Asn Leu Val Met Tyr Ile Val Ile Ile Ile His Trp
109          300          305          310
111 aat gca tgt gtg ttc tac tct att tct aaa gct att gga ttt gga aat      1011
112 Asn Ala Cys Val Phe Tyr Ser Ile Ser Lys Ala Ile Gly Phe Gly Asn
113          315          320          325
115 gat aca tgg gtc tac cct gat att aat gat cct gaa ttt ggc cgt ttg      1059
116 Asp Thr Trp Val Tyr Pro Asp Ile Asn Asp Pro Glu Phe Gly Arg Leu
117 330          335          340          345
119 gct aga aaa tac gta tac agc ctt tac tgg tct aca ctg act ttg act      1107
120 Ala Arg Lys Tyr Val Tyr Ser Leu Tyr Trp Ser Thr Leu Thr Leu Thr
121          350          355          360
123 acc att ggt gaa aca ccc cct ccc gtg agg gat tct gag tat gtc ttt      1155
124 Thr Ile Gly Glu Thr Pro Pro Pro Val Arg Asp Ser Glu Tyr Val Phe

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125		365		370		375		
127	gtg	gtg	ggt	gat	ttc	cta	att	gga
128	Val	Val	Val	Asp	Phe	Leu	Ile	Gly
129								
131	ggt	aac	ata	ggt	tct	atg	att	tcc
132	Gly	Asn	Ile	Gly	Ser	Met	Ile	Ser
133								
135	ttt	caa	gca	aga	att	gat	gct	atc
136	Phe	Gln	Ala	Arg	Ile	Asp	Ala	Ile
137	410							
139	gta	agc	aaa	gat	atg	gaa	aag	agg
140	Val	Ser	Lys	Asp	Met	Glu	Lys	Arg
141								
143	tgg	acc	aac	aaa	aaa	aca	ggt	gat
144	Trp	Thr	Asn	Lys	Lys	Thr	Val	Asp
145								
147	cct	gat	aaa	cta	aga	gca	gaa	att
148	Pro	Asp	Lys	Leu	Arg	Ala	Glu	Ile
149								
151	tta	aaa	aag	gta	cgc	att	ttt	gct
152	Leu	Lys	Lys	Val	Arg	Ile	Phe	Ala
153								
155	gag	ttg	gtc	ttg	aaa	ttg	caa	ccc
156	Glu	Leu	Val	Leu	Lys	Leu	Gln	Pro
157	490							
159	att	tgc	aag	aaa	ggg	gat	atc	gga
160	Ile	Cys	Lys	Lys	Gly	Asp	Ile	Gly
161								
163	ggc	aaa	ctc	gct	gtg	gtg	gca	gat
164	Gly	Lys	Leu	Ala	Val	Val	Ala	Asp
165								
167	ttg	agc	gat	ggc	agc	acc	ttc	ggt
168	Leu	Ser	Asp	Gly	Ser	Thr	Phe	Gly
169								
171	ggg	agc	aaa	gct	ggc	aat	cga	aga
172	Gly	Ser	Lys	Ala	Gly	Asn	Arg	Thr
173								
175	tac	tca	gac	ctg	ttc	tgt	ctc	tca
176	Tyr	Ser	Asp	Leu	Phe	Cys	Leu	Ser
177	570							
179	act	gag	tac	cca	gat	gcc	aaa	act
180	Thr	Glu	Tyr	Pro	Asp	Ala	Lys	Thr
181								
183	att	tta	atg	aaa	gat	ggt	cta	ctg
184	Ile	Leu	Met	Lys	Asp	Gly	Leu	Leu
185								
187	agt	gat	cct	aaa	gat	ctt	gaa	gag
188	Ser	Asp	Pro	Lys	Asp	Leu	Glu	Glu
189								

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191 gta gac ctc ctg caa acc agg ttt gcc cga atc ttg gct gag tat gag      1971
192 Val Asp Leu Leu Gln Thr Arg Phe Ala Arg Ile Leu Ala Glu Tyr Glu
193      635                      640                      645
195 tcc atg cag cag aaa ctg aaa caa aga tta acc aag gtt gag aaa ttt      2019
196 Ser Met Gln Gln Lys Leu Lys Gln Arg Leu Thr Lys Val Glu Lys Phe
197 650                      655                      660                      665
199 ctg aaa ccg ctt att gac aca gaa ttt tca agt att gag gga cct tgg      2067
200 Leu Lys Pro Leu Ile Asp Thr Glu Phe Ser Ser Ile Glu Gly Pro Trp
201      670                      675                      680
203 agc gaa agt ggg ccc atc gac tct aca tag aaccgaaaag ctgggtcatta      2117
204 Ser Glu Ser Gly Pro Ile Asp Ser Thr
205      685                      690
207 acagggacat gcctcatgat ccttttgatc ctatgactga catcaactaa aattttaaaag      2177
209 aagaggaaga ctacagttggg aaatttttcc atgaggaaaa tgtgcttttg tgcaagggtac      2237
211 agcccacacc tctctgagag atactatgat taaaaaagct ttatatctgg gatttttcac      2297
213 aactgataat gtgcaaagat ataaactgat taacttgatca gtgtctgtat tttctgattt      2357
215 tttcacatac gctcatttta tgtaatatcc ttcataaaaa tgaataagta gccctcactt      2417
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223 <211> LENGTH: 690
224 <212> TYPE: PRT
225 <213> ORGANISM: homo sapiens
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234      20      25      30
237 Arg Met Glu Asn Gly Ala Cys Ser Ser Phe Ser Glu Asp Asp Asp Ser
238      35      40      45
241 Ala Tyr Thr Ser Glu Glu Ser Glu Asn Glu Asn Pro His Ala Arg Gly
242      50      55      60
245 Ser Phe Ser Tyr Lys Ser Leu Arg Lys Gly Gly Pro Ser Gln Arg Glu
246 65      70      75      80
249 Gln Tyr Leu Pro Gly Ala Ile Ala Ile Phe Asn Val Asn Asn Ser Ser
250      85      90      95
253 Asn Lys Asp Gln Glu Pro Glu Glu Lys Lys Lys Lys Lys Lys Glu Lys
254      100     105     110
257 Lys Ser Lys Ser Asp Asp Lys Asn Glu Asn Lys Asn Asp Pro Glu Lys
258      115     120     125
261 Lys Lys Lys Lys Lys Asp Lys Glu Lys Lys Lys Lys Glu Glu Lys Ser
262      130     135     140
265 Lys Asp Lys Lys Glu His His Lys Lys Glu Val Val Val Ile Asp Pro
266 145     150     155     160
269 Ser Gly Asn Thr Tyr Tyr Asn Trp Leu Phe Cys Ile Thr Leu Pro Val
270      165     170     175
273 Met Tyr Asn Trp Thr Met Val Ile Ala Arg Ala Cys Phe Asp Glu Leu
274      180     185     190
277 Gln Ser Asp Tyr Leu Glu Tyr Trp Leu Ile Leu Asp Tyr Val Ser Asp

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278          195          200          205
281 Ile Val Tyr Leu Ile Asp Met Phe Val Arg Thr Arg Thr Gly Tyr Leu
282          210          215          220
285 Glu Gln Gly Leu Leu Val Lys Glu Glu Leu Lys Leu Ile Asn Lys Tyr
286 225          230          235          240
289 Lys Ser Asn Leu Gln Phe Lys Leu Asp Val Leu Ser Leu Ile Pro Thr
290          245          250          255
293 Asp Leu Leu Tyr Phe Lys Leu Gly Trp Asn Tyr Pro Glu Ile Arg Leu
294          260          265          270
297 Asn Arg Leu Leu Arg Phe Ser Arg Met Phe Glu Phe Phe Gln Arg Thr
298          275          280          285
301 Glu Thr Arg Thr Asn Tyr Pro Asn Ile Phe Arg Ile Ser Asn Leu Val
302          290          295          300
305 Met Tyr Ile Val Ile Ile Ile His Trp Asn Ala Cys Val Phe Tyr Ser
306 305          310          315          320
309 Ile Ser Lys Ala Ile Gly Phe Gly Asn Asp Thr Trp Val Tyr Pro Asp
310          325          330          335
313 Ile Asn Asp Pro Glu Phe Gly Arg Leu Ala Arg Lys Tyr Val Tyr Ser
314          340          345          350
317 Leu Tyr Trp Ser Thr Leu Thr Leu Thr Thr Ile Gly Glu Thr Pro Pro
318          355          360          365
321 Pro Val Arg Asp Ser Glu Tyr Val Phe Val Val Val Asp Phe Leu Ile
322          370          375          380
325 Gly Val Leu Ile Phe Ala Thr Ile Val Gly Asn Ile Gly Ser Met Ile
326 385          390          395          400
329 Ser Asn Met Asn Ala Ala Arg Ala Glu Phe Gln Ala Arg Ile Asp Ala
330          405          410          415
333 Ile Lys Gln Tyr Met His Phe Arg Asn Val Ser Lys Asp Met Glu Lys
334          420          425          430
337 Arg Val Ile Lys Trp Phe Asp Tyr Leu Trp Thr Asn Lys Lys Thr Val
338          435          440          445
341 Asp Glu Lys Glu Val Leu Lys Tyr Leu Pro Asp Lys Leu Arg Ala Glu
342          450          455          460
345 Ile Ala Ile Asn Val His Leu Asp Thr Leu Lys Lys Val Arg Ile Phe
346 465          470          475          480
349 Ala Asp Cys Glu Ala Gly Leu Leu Val Glu Leu Val Leu Lys Leu Gln
350          485          490          495
353 Pro Gln Val Tyr Ser Pro Gly Asp Tyr Ile Cys Lys Lys Gly Asp Ile
354          500          505          510
357 Gly Arg Glu Met Tyr Ile Ile Lys Glu Gly Lys Leu Ala Val Val Ala
358          515          520          525
361 Asp Asp Gly Val Thr Gln Phe Val Val Leu Ser Asp Gly Ser Thr Phe
362          530          535          540
365 Gly Glu Ile Ser Ile Leu Asn Ile Lys Gly Ser Lys Ala Gly Asn Arg
366 545          550          555          560
369 Arg Thr Ala Asn Ile Lys Ser Ile Gly Tyr Ser Asp Leu Phe Cys Leu
370          565          570          575
373 Ser Lys Asp Asp Leu Met Glu Ala Leu Thr Glu Tyr Pro Asp Ala Lys
374          580          585          590

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RAW SEQUENCE LISTING ERROR SUMMARY
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

VERIFICATION SUMMARY

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L:7 M:283 W: Missing Blank Line separator, <130> field identifier

L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date